



Docket No. CDS-237

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Jian Zheng Confirmation No.: 6987
Appln. No. : 09/823,077
Filed : March 30, 2001
Title : Novel Hepatitis B Virus
Art Unit : 1648
Examiner : Laurie A. Scheiner

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May 31, 2005

(Date of Deposit)

Stacey B. Antar

(Name of applicant, assignee, or Registered Representative)

(Signature)

May 31, 2005

(Date of Signature)

Mail Stop Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

AMENDMENT

Dear Sir:

In response to the notice to comply with requirements for a patent application containing nucleotide sequence and/or amino acid sequence disclosures mailed December 01, 2004, the Applicant hereby submits a Petition for an Extension of Time and a corrected Sequence Listing and this accompanying amendment. Please amend the above-identified application as follows:

Amendments to the Specification begin on page 2 of this paper.

Amendments to the Claims begin on page 4 of this paper.

Remarks begin on page 5 of this paper.

A corrected Sequence Listing is attached following page 5 of this paper.

Amendments to the Specification:

Please replace the paragraph beginning at page 5, line 1 with the following rewritten paragraph:

First-round Primer Set:

F1-6 (231-252): SEQ.ID. NO.: 1 CCTCACAATACCGCAGAGTCTA

R1-6 (816-842): SEQ.ID. NO.: 2 AGGGTTTAAATGTATACCCAAAGACAA

Second-round Primer Set:

F1-7 (246-268): SEQ.ID. NO.: 3 GAGTCTAGACTCGTGTTGGACTT

R13-2d (822-843): SEQ.ID. NO.: 4 CCGAATTCTAGGGTTTAAATGTATACCCA

An EcoR I site was added at the 5'-end of R13-2d for cloning purpose.--

Please replace the paragraph beginning at page 8, line 6 with the following rewritten paragraph:

Example 5: HBs Variant DNA Sequence and Amino Acid Sequence Analysis

The HBs DNA sequence of this novel Lebanese (LBN) variant was analyzed for genotypes. Sequence comparison between variant HBs DNA sequence and other 28 defined HBs genotype strain put this variant HBs into genotype D group (Fig. 1). Although serological typing on this patient's serum was not performed, the amino acid sequence of this HBs variant showed highest homology with ayw2 HBs subtype. Five amino acid mutations within position 32-226 of LBN variant were observed in all five clones. They are 103 M (ATG)→ I (ATT) , 118 T (ACG)→ K (AAG), 120 P (CCA) → Q (CAA), 170 175 L (TTA)→ S (TCA) and 213 L (TTA) → S (TCA), as shown in SEQ.ID.NO.: 7. At amino acid position 122, three clones revealed sequence Arg (AGA) while 2 clones revealed sequence as Lys (AAA). }- For recombinant LBN HBsAg expression, sequence with Arg (122) was used.

Please replace the paragraph beginning at page 8, line 23 with the following rewritten paragraph:

-- 102 - 110 - 120 - 130 - 140 - 150

SEQ.ID. NO.: 5

wt (ayw2) GMLPVCPLIPGSSTTSTGPCRT**CTTPAQG**TSMY**PSCCCTKPSD**GNCTCI

SEQ.ID. NO.: 6

 LBN -I-----K-Q-----

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